



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/963761  
Source: O I P E  
Date Processed by STIC: 10/10/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/963761
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPIA" HEADERS, WHICH WERE INSERTED BY PTO		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

AMC/MH - Biotechnology Systems Branch - 08/21/2001

Errored: ① Input 33; Found 25

② Sequences are misordered/misnumbered

OIPE

## RAW SEQUENCE LISTING

DATE: 10/10/2001

PATENT APPLICATION: US/09/963,761

TIME: 14:20:54

Input Set : A:\ES.txt

Output Set: N:\CRF3\10102001\I963761.raw

## SEQUENCE LISTING

2 (1) GENERAL INFORMATION:  
 3 (i) APPLICANT: TZAHI ARAZI, YOEL MOSHE SHIBOLETH  
 4 AND AMIT GAL-ON  
 5 (ii) TITLE OF INVENTION: VECTORS FOR EXPRESSING HETEROLOGOUS  
 6 PEPTIDES  
 7 AT THE AMINO-TERMINUS OF POTYVIRUS COAT  
 8 Protein, methods for use thereof, plants infected with  
 same and methods of  
 W--> 9 vaccination using same *OK*  
 11 (iii) NUMBER OF SEQUENCES: 33  
 13 (iv) CORRESPONDENCE ADDRESS:  
 14 (A) ADDRESSEE: Mark M. Friedman C/O Mr. Bill Polkinghorn  
 15 Discovery Dispatch  
 16 (B) STREET: 9003 Florin Way  
 17 (C) CITY: Upper Marlboro  
 18 (D) STATE: Maryland  
 19 (E) COUNTRY: United States of America  
 20 (F) ZIP: 20772  
 21 (v) COMPUTER READABLE FORM:  
 22 (A) MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
 23 (B) COMPUTER: Twinhead\* Slimnote-890TX  
 24 (C) OPERATING SYSTEM: MS DOS version 6.2,  
 25 Windows version 3.11  
 26 (D) SOFTWARE: Word for Windows version 2.0 converted to  
 27 an ASCII file  
 28 (vi) CURRENT APPLICATION DATA:  
 C--> 29 (A) APPLICATION NUMBER: US/09/963,761 *OK*  
 C--> 30 (B) FILING DATE: 27-Sep-2001  
 31 (C) CLASSIFICATION: XXX  
 32 (vii) PRIOR APPLICATION DATA:  
 33 (A) APPLICATION NUMBER: 60/253,136  
 34 (B) FILING DATE: 28 November, 2000  
 C--> 35 (A) APPLICATION NUMBER:  
 C--> 36 (B) FILING DATE:  
 C--> 37 (A) APPLICATION NUMBER: *OK*  
 C--> 38 (B) FILING DATE:  
 39 (viii) ATTORNEY/AGENT INFORMATION:  
 40 (A) NAME: Friedmam, Mark M.  
 41 (B) REGISTRATION NUMBER: 33,883  
 42 (C) REFERENCE/DOCKET NUMBER: 1686/4  
 43 (ix) TELECOMMUNICATION INFORMATION:  
 44 (A) TELEPHONE: 972-3-5625553  
 45 (B) TELEFAX: 972-3-5625554  
 46 (C) TELEX:

Does Not Comply  
 Corrected Diskette Needed

① Input 33; Found 25  
 ② Sequences are misordered/  
 misnumbered

*Errors*

Input 33 Found ~~25~~ 25  
 Sequences misnumbered

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/963,761

DATE: 10/10/2001  
TIME: 14:20:54

Input Set : A:\ES.txt  
Output Set: N:\CRF3\10102001\I963761.raw

## ERRORED SEQUENCES

121 (2) INFORMATION FOR SEQ ID NO: 3:  
122 (i) SEQUENCE CHARACTERISTICS:  
123 (A) LENGTH: 20  
124 (B) TYPE: nucleic acid  
125 (C) STRANDEDNESS: Single  
126 (D) TOPOLOGY: linear  
127 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
130 CATTTCCTTT CACGCGTGGC 20  
E--> 132 (2) INFORMATION FOR SEQ ID NO:4:  
132 (2) INFORMATION FOR SEQ ID NO: 4:  
133 (i) SEQUENCE CHARACTERISTICS:  
134 (A) LENGTH: 21  
135 (B) TYPE: nucleic acid  
136 (C) STRANDEDNESS: Single  
137 (D) TOPOLOGY: linear  
138 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
140 TCACACCATC ACCATCACCA T  
E--> 142 (2) INFORMATION FOR SEQ ID NO:5:  
153 (2) INFORMATION FOR SEQ ID NO: 6:  
154 (i) SEQUENCE CHARACTERISTICS:  
155 (A) LENGTH: 53  
156 (B) TYPE: nucleic acid  
157 (C) STRANDEDNESS: Single  
158 (D) TOPOLOGY: linear  
159 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
161 CAGCTGCAGT CACACCATCA CCATCACCAT TCAGGCACTC AGCCAACTGT 50  
162 GGC  
E--> 165 (2) INFORMATION FOR SEQ ID NO:7:  
165 (2) INFORMATION FOR SEQ ID NO: 7:  
166 (i) SEQUENCE CHARACTERISTICS:  
167 (A) LENGTH: 55  
168 (B) TYPE: nucleic acid  
169 (C) STRANDEDNESS: Single  
170 (D) TOPOLOGY: linear  
171 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
173 CAGCTGCAGT CACACCATCA CCATCACCAT GATACTGGAG CTACAAAGAA 50  
174 AGAAG  
E--> 176 (2) INFORMATION FOR SEQ ID NO:8:  
176 (2) INFORMATION FOR SEQ ID NO: 8:  
177 (i) SEQUENCE CHARACTERISTICS:  
178 (A) LENGTH: 55  
179 (B) TYPE: nucleic acid  
180 (C) STRANDEDNESS: Single  
181 (D) TOPOLOGY: linear  
182 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
184 TCAGCATCAG AGCAGAAGCT CATTTCAGAG GAGGATCTCG GATCC 45  
E--> 186 (2) INFORMATION FOR SEQ ID NO:9:  
186 (2) INFORMATION FOR SEQ ID NO: 9:

(21)

sequences not numbered

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

(53)

(55)

(45)

Errored Input 55  
Found 95

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/963,761

DATE: 10/10/2001

TIME: 14:20:54

Input Set : A:\ES.txt

Output Set: N:\CRF3\10102001\I963761.raw

187 (i) SEQUENCE CHARACTERISTICS:  
 188 (A) LENGTH: 15  
 189 (B) TYPE: amino acid  
 190 (C) STRANDEDNESS: single  
 191 (D) TOPOLOGY: linear  
 192 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
 193 Ser Ala Ser Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Gly Ser  
 E--> 194 5 10  
 196 (2) INFORMATION FOR SEQ ID NO: 10:  
 196 (2) INFORMATION FOR SEQ ID NO: 10:  
 197 (i) SEQUENCE CHARACTERISTICS:  
 198 (A) LENGTH: 77  
 199 (B) TYPE: nucleic acid  
 200 (C) STRANDEDNESS: Single  
 201 (D) TOPOLOGY: linear  
 202 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
 204 CAGCTGCACT CAGCATCAGA GCAGAAGCTC ATTTTCAGAGG AGGATCTCGG 50  
 205 ATCCTCAGGC ACTCAGCCAA CTGTGGC 77  
 E--> 208 (2) INFORMATION FOR SEQ ID NO: 11:  
 208 (2) INFORMATION FOR SEQ ID NO: 11:  
 209 (i) SEQUENCE CHARACTERISTICS:  
 210 (A) LENGTH: 82  
 211 (B) TYPE: nucleic acid  
 212 (C) STRANDEDNESS: Single  
 213 (D) TOPOLOGY: linear  
 E--> 214 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:  
 216 CAGCTGCACT CAGCATCAGA GCAGAAGCTC ATTTTCAGAGG AGGATCTCGG 50  
 217 ATCCGATACT GGAGCTACAA AGAAAGATAA AG 82  
 E--> 219 (2) INFORMATION FOR SEQ ID NO: 12:  
 219 (2) INFORMATION FOR SEQ ID NO: 12:  
 220 (i) SEQUENCE CHARACTERISTICS:  
 221 (A) LENGTH: 81  
 222 (B) TYPE: nucleic acid  
 223 (C) STRANDEDNESS: Single  
 224 (D) TOPOLOGY: linear  
 225 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
 227 CAGCTGCACT CAGCATCAGA GCAGAAGCTC ATTTTCAGAGG AGGATCTCGG 50  
 228 ATCCAAGAAA GATAAAGAAG ATGACAAAGG G 81  
 E--> 230 (2) INFORMATION FOR SEQ ID NO: 13:  
 230 (2) INFORMATION FOR SEQ ID NO: 13:  
 231 (i) SEQUENCE CHARACTERISTICS:  
 232 (A) LENGTH: 81  
 233 (B) TYPE: nucleic acid  
 234 (C) STRANDEDNESS: Single  
 235 (D) TOPOLOGY: linear  
 E--> 236 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:  
 238 CGCGGATCCG ATGACAAAGG GAAAAACAAG G 81  
 E--> 241 (2) INFORMATION FOR SEQ ID NO: 14:  
 241 (2) INFORMATION FOR SEQ ID NO: 14:

Input 15  
 Found 14  
 (15)

Sequences  
 misordered

Sequences  
 misordered

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/963,761

DATE: 10/10/2001  
TIME: 14:20:54

Input Set : A:\ES.txt  
Output Set: N:\CRF3\10102001\I963761.raw

242 (i) SEQUENCE CHARACTERISTICS:  
243 (A) LENGTH: 30  
244 (B) TYPE: nucleic acid  
245 (C) STRANDEDNESS: Single  
246 (D) TOPOLOGY: linear  
247 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
249 CTCGGATCCA ACAAGGATGT TACAGGCTCC  
E--> 251 (2) INFORMATION FOR SEQ ID NO: 15: 30  
251 (2) INFORMATION FOR SEQ ID NO: 15: — sequences unordered  
252 (i) SEQUENCE CHARACTERISTICS:  
253 (A) LENGTH: 27  
254 (B) TYPE: nucleic acid  
255 (C) STRANDEDNESS: Single  
256 (D) TOPOLOGY: linear  
257 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
259 CGCGGATCCG GCTCCGGCTC AAGTGAG 27  
E--> 261 (2) INFORMATION FOR SEQ ID NO: 16:  
261 (2) INFORMATION FOR SEQ ID NO: 16:  
262 (i) SEQUENCE CHARACTERISTICS:  
263 (A) LENGTH: 30  
264 (B) TYPE: nucleic acid  
265 (C) STRANDEDNESS: Single  
266 (D) TOPOLOGY: linear  
267 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
269 CGCGGATCCG AGAAAACAGT GGCAGCTGTC 30  
E--> 271 (2) INFORMATION FOR SEQ ID NO: 17:  
271 (2) INFORMATION FOR SEQ ID NO: 17:  
272 (i) SEQUENCE CHARACTERISTICS:  
273 (A) LENGTH: 28  
274 (B) TYPE: nucleic acid  
275 (C) STRANDEDNESS: Single  
276 (D) TOPOLOGY: linear  
277 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
279 CGCGGATCCG CTGTCACGAA GGACAAGG 28  
E--> 281 (2) INFORMATION FOR SEQ ID NO: 18:  
281 (2) INFORMATION FOR SEQ ID NO: 18:  
282 (i) SEQUENCE CHARACTERISTICS:  
283 (A) LENGTH: 33  
284 (B) TYPE: nucleic acid  
285 (C) STRANDEDNESS: Single  
286 (D) TOPOLOGY: linear  
287 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
289 CGCGGATCCA AGGATGTAAA TGCTGGTTCT CAT 33  
E--> 291 (2) INFORMATION FOR SEQ ID NO: 19:  
291 (2) INFORMATION FOR SEQ ID NO: 19:  
292 (i) SEQUENCE CHARACTERISTICS:  
293 (A) LENGTH: 30  
294 (B) TYPE: nucleic acid  
295 (C) STRANDEDNESS: Single

## RAW SEQUENCE LISTING

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296         (D) TOPOLOGY: linear
297         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:
299 CTCGGATCCG GTTCTCATGG GAAAATTGTG
E--> 301 (2) INFORMATION FOR SEQ ID NO: 20:
301 (2) INFORMATION FOR SEQ ID NO: 20:
302         (i) SEQUENCE CHARACTERISTICS:
303             (A) LENGTH: 51
304             (B) TYPE: nucleic acid
305             (C) STRANDEDNESS: Single
306             (D) TOPOLOGY: linear
307         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:
309 AGTGTGAGAG GAGATCTTCA AGTGCTTGCA CGAAAAGCAG CAAGACCACT 50
310 T
E--> 312 (2) INFORMATION FOR SEQ ID NO: 21:
312 (2) INFORMATION FOR SEQ ID NO: 21:
313         (i) SEQUENCE CHARACTERISTICS:
314             (A) LENGTH: 17
315             (B) TYPE: amino acid
316             (C) STRANDEDNESS: single
317             (D) TOPOLOGY: linear
318         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:
320 Ser Val Arg Gly Asp Leu Gln Val Leu Ala Arg Lys Ala Ala Arg
E--> 321          5              10              15
322 Pro Leu
323     17
325 (2) INFORMATION FOR SEQ ID NO: 22:
325 (2) INFORMATION FOR SEQ ID NO: 22:
326         (i) SEQUENCE CHARACTERISTICS:
327             (A) LENGTH: 87
328             (B) TYPE: nucleic acid
329             (C) STRANDEDNESS: Single
330             (D) TOPOLOGY: linear
331         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:
333 CAGCTGCAGT CCGTGAGAGG AGATCTTCAA GTGCTTGAC GAAAAGCAGC 50
334 AAGACCACTT AAGAAAGATA AAGAAGATGA CAAAGGG
E--> 336 (2) INFORMATION FOR SEQ ID NO: 23:
336 (2) INFORMATION FOR SEQ ID NO: 23:
337         (i) SEQUENCE CHARACTERISTICS:
338             (A) LENGTH: 83
339             (B) TYPE: nucleic acid
340             (C) STRANDEDNESS: Single
341             (D) TOPOLOGY: linear
342         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:
344 CAGCTGCAGA GTGTGAGAGG AGATCTTCAA GTGCTTGAC GAAAAGCAGC 50
345 AAGACCACTT TCAGGCACTC AGCCAAGTGT GGC
E--> 348 (2) INFORMATION FOR SEQ ID NO: 24:
348 (2) INFORMATION FOR SEQ ID NO: 24:
349         (i) SEQUENCE CHARACTERISTICS:
350             (A) LENGTH: 84

```

sequences misordered

## RAW SEQUENCE LISTING

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Input Set : A:\ES.txt

Output Set: N:\CRF3\10102001\I963761.raw

```

351          (B) TYPE: nucleic acid
352          (C) STRANDEDNESS: Single
353          (D) TOPOLOGY: linear
354          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:
356 CGCGGATCCG TGAGAGGAGA TCTTCAAGTG CTTGCACGAA AAGCAGCAAG 50
357 ACCACTTAAG AAAGATAAAG AAGATGACAA AGGG                84
E--> 359 (2) INFORMATION FOR SEQ ID NO:25:
359 (2) INFORMATION FOR SEQ ID NO: 25:
360          (i) SEQUENCE CHARACTERISTICS:
361              (A) LENGTH: 33
362              (B) TYPE: nucleic acid
363              (C) STRANDEDNESS: Single
364              (D) TOPOLOGY: linear
365          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:
367 CAGCTGCAGT CCGAGAAAAC AGTGGCAGCT GTC
E--> 369 (2) INFORMATION FOR SEQ ID NO: 26?
399 (2) INFORMATION FOR SEQ ID NO: 29:
400          (i) SEQUENCE CHARACTERISTICS:
401              (A) LENGTH: 8
402              (B) TYPE: amino acid
403              (C) STRANDEDNESS: single
404              (D) TOPOLOGY: linear
405          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:
407 Ser Ile Ile Asn Phe Glu Lys Leu
E--> 408
410 (2) INFORMATION FOR SEQ ID NO:30:

```

33  
sequences misnumbered

5  
misaligned amino numbering  
counted as read as  
end of file identifier



## VERIFICATION SUMMARY

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Input Set : A:\ES.txt

Output Set: N:\CRF3\10102001\I963761.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:9 M:259 W: Allowed number of lines exceeded, (ii) TITLE OF INVENTION:  
L:35 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:36 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:37 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:38 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:132 M:254 E: No. of Bases conflict, Input:0 Counted:30 SEQ:3  
L:132 M:320 E: (1) Wrong Nucleic Acid Designator, 17  
L:132 M:204 E: No. of Bases differ, LENGTH:Input:20 Counted:45 SEQ:3  
L:142 M:254 E: No. of Bases conflict, Input:0 Counted:31 SEQ:4  
L:142 M:320 E: (1) Wrong Nucleic Acid Designator, 17  
L:142 M:204 E: No. of Bases differ, LENGTH:Input:21 Counted:46 SEQ:4  
L:165 M:254 E: No. of Bases conflict, Input:0 Counted:63 SEQ:6  
L:165 M:320 E: (1) Wrong Nucleic Acid Designator, 17  
L:165 M:204 E: No. of Bases differ, LENGTH:Input:53 Counted:78 SEQ:6  
L:176 M:254 E: No. of Bases conflict, Input:0 Counted:65 SEQ:7  
L:176 M:320 E: (1) Wrong Nucleic Acid Designator, 17  
L:176 M:204 E: No. of Bases differ, LENGTH:Input:55 Counted:80 SEQ:7  
L:186 M:254 E: No. of Bases conflict, Input:0 Counted:55 SEQ:8  
L:186 M:320 E: (1) Wrong Nucleic Acid Designator, 17  
L:186 M:204 E: No. of Bases differ, LENGTH:Input:55 Counted:70 SEQ:8  
L:194 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9  
L:208 M:254 E: No. of Bases conflict, Input:0 Counted:87 SEQ:10  
L:208 M:320 E: (1) Wrong Nucleic Acid Designator, 18  
L:208 M:204 E: No. of Bases differ, LENGTH:Input:77 Counted:102 SEQ:10  
L:214 M:202 E: (16) Value must be an Integer, Data=[x:]  
L:219 M:254 E: No. of Bases conflict, Input:0 Counted:92 SEQ:11  
L:219 M:320 E: (1) Wrong Nucleic Acid Designator, 18  
L:219 M:204 E: No. of Bases differ, LENGTH:Input:82 Counted:107 SEQ:11  
L:230 M:254 E: No. of Bases conflict, Input:0 Counted:91 SEQ:12  
L:230 M:320 E: (1) Wrong Nucleic Acid Designator, 18  
L:230 M:204 E: No. of Bases differ, LENGTH:Input:81 Counted:106 SEQ:12  
L:236 M:202 E: (16) Value must be an Integer, Data=[x:]  
L:241 M:254 E: No. of Bases conflict, Input:0 Counted:41 SEQ:13  
L:241 M:320 E: (1) Wrong Nucleic Acid Designator, 18  
L:241 M:204 E: No. of Bases differ, LENGTH:Input:31 Counted:56 SEQ:13  
L:251 M:254 E: No. of Bases conflict, Input:0 Counted:40 SEQ:14  
L:251 M:320 E: (1) Wrong Nucleic Acid Designator, 18  
L:251 M:204 E: No. of Bases differ, LENGTH:Input:30 Counted:55 SEQ:14  
L:261 M:254 E: No. of Bases conflict, Input:0 Counted:37 SEQ:15  
L:261 M:320 E: (1) Wrong Nucleic Acid Designator, 18  
L:261 M:204 E: No. of Bases differ, LENGTH:Input:27 Counted:52 SEQ:15  
L:271 M:254 E: No. of Bases conflict, Input:0 Counted:40 SEQ:16  
L:271 M:320 E: (1) Wrong Nucleic Acid Designator, 18  
L:271 M:204 E: No. of Bases differ, LENGTH:Input:30 Counted:55 SEQ:16  
L:281 M:254 E: No. of Bases conflict, Input:0 Counted:38 SEQ:17  
L:281 M:320 E: (1) Wrong Nucleic Acid Designator, 18

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/963,761

DATE: 10/10/2001

TIME: 14:20:55

Input Set : A:\ES.txt

Output Set: N:\CRF3\10102001\I963761.raw

L:281 M:204 E: No. of Bases differ, LENGTH:Input:28 Counted:53 SEQ:17  
L:291 M:254 E: No. of Bases conflict, Input:0 Counted:43 SEQ:18  
L:291 M:320 E: (1) Wrong Nucleic Acid Designator, 18  
L:291 M:204 E: No. of Bases differ, LENGTH:Input:33 Counted:58 SEQ:18  
L:301 M:254 E: No. of Bases conflict, Input:0 Counted:40 SEQ:19  
L:301 M:320 E: (1) Wrong Nucleic Acid Designator, 18  
L:301 M:204 E: No. of Bases differ, LENGTH:Input:30 Counted:55 SEQ:19  
L:312 M:254 E: No. of Bases conflict, Input:0 Counted:61 SEQ:20  
L:312 M:320 E: (1) Wrong Nucleic Acid Designator, 18  
L:312 M:204 E: No. of Bases differ, LENGTH:Input:51 Counted:76 SEQ:20  
L:321 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:21  
L:336 M:254 E: No. of Bases conflict, Input:0 Counted:97 SEQ:22  
L:336 M:320 E: (1) Wrong Nucleic Acid Designator, 18  
L:336 M:204 E: No. of Bases differ, LENGTH:Input:87 Counted:112 SEQ:22  
L:348 M:254 E: No. of Bases conflict, Input:0 Counted:93 SEQ:23  
L:348 M:320 E: (1) Wrong Nucleic Acid Designator, 18  
L:348 M:204 E: No. of Bases differ, LENGTH:Input:83 Counted:108 SEQ:23  
L:359 M:254 E: No. of Bases conflict, Input:0 Counted:94 SEQ:24  
L:359 M:320 E: (1) Wrong Nucleic Acid Designator, 18  
L:359 M:204 E: No. of Bases differ, LENGTH:Input:84 Counted:109 SEQ:24  
L:369 M:254 E: No. of Bases conflict, Input:0 Counted:43 SEQ:25  
L:369 M:320 E: (1) Wrong Nucleic Acid Designator, 18  
L:369 M:204 E: No. of Bases differ, LENGTH:Input:33 Counted:58 SEQ:25  
L:379 M:254 E: No. of Bases conflict, Input:0 Counted:44 SEQ:26  
L:379 M:320 E: (1) Wrong Nucleic Acid Designator, 18  
L:379 M:204 E: No. of Bases differ, LENGTH:Input:34 Counted:59 SEQ:26  
L:389 M:254 E: No. of Bases conflict, Input:0 Counted:47 SEQ:27  
L:389 M:320 E: (1) Wrong Nucleic Acid Designator, 18  
L:389 M:204 E: No. of Bases differ, LENGTH:Input:37 Counted:62 SEQ:27  
L:399 M:254 E: No. of Bases conflict, Input:0 Counted:34 SEQ:28  
L:399 M:320 E: (1) Wrong Nucleic Acid Designator, 18  
L:399 M:204 E: No. of Bases differ, LENGTH:Input:24 Counted:49 SEQ:28  
L:408 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:29  
L:421 M:254 E: No. of Bases conflict, Input:0 Counted:66 SEQ:30  
L:421 M:320 E: (1) Wrong Nucleic Acid Designator, 18  
L:421 M:204 E: No. of Bases differ, LENGTH:Input:56 Counted:81 SEQ:30  
L:433 M:254 E: No. of Bases conflict, Input:0 Counted:43 SEQ:31  
L:433 M:320 E: (1) Wrong Nucleic Acid Designator, 18  
L:433 M:204 E: No. of Bases differ, LENGTH:Input:56 Counted:58 SEQ:31  
L:444 M:254 E: No. of Bases conflict, Input:0 Counted:32 SEQ:32  
L:444 M:320 E: (1) Wrong Nucleic Acid Designator, 18  
L:444 M:204 E: No. of Bases differ, LENGTH:Input:22 Counted:47 SEQ:32